

SCORE Search Results Details for Application 10568108 and Search Result 20070629_130903_us-10-568-108-2.rag.

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This page gives you Search Results detail for the Application 10568108 and Search Result 20070629_130903_us-10-568-108-2.rag.

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OM protein - protein search, using sw model

Run on: June 30, 2007, 00:44:29 ; Search time 260 Seconds
(without alignments)
41.405 Million cell updates/sec

Title: US-10-568-108-2
Perfect score: 109
Sequence: 1 GAYDLRRRERQSRLRRRERQSR 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_200701:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

9: geneseqp2005s:*

10: geneseqp2006s:*

11: geneseqp2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query Score | Match | Length | DB | ID | Description |
|------------|-------------|-------|--------|----|----|-------------|
|------------|-------------|-------|--------|----|----|-------------|

| | | | | | | |
|----|-----|-------|-----|----|----------|--------------------|
| 1 | 109 | 100.0 | 22 | 9 | ADY21199 | Ady21199 Human cel |
| 2 | 109 | 100.0 | 22 | 9 | ADY21241 | Ady21241 Gram-nega |
| 3 | 109 | 100.0 | 22 | 9 | ADY29688 | Ady29688 Antibacte |
| 4 | 109 | 100.0 | 23 | 9 | ADY21209 | Ady21209 Human cel |
| 5 | 66 | 60.6 | 22 | 9 | ADY21246 | Ady21246 Gram-nega |
| 6 | 66 | 60.6 | 22 | 9 | ADY29693 | Ady29693 Antibacte |
| 7 | 66 | 60.6 | 197 | 1 | AAP91931 | Aap91931 Human hep |
| 8 | 66 | 60.6 | 199 | 7 | ADF17970 | Adf17970 Human cat |
| 9 | 66 | 60.6 | 199 | 7 | ADG42089 | Adg42089 Human cor |
| 10 | 66 | 60.6 | 200 | 8 | ABM84641 | Abm84641 Human dia |
| 11 | 66 | 60.6 | 221 | 2 | AAR84663 | Aar84663 Human hep |
| 12 | 66 | 60.6 | 221 | 2 | AAW04875 | Aaw04875 Heparin b |
| 13 | 66 | 60.6 | 222 | 2 | AAR41935 | Aar41935 Recombina |
| 14 | 66 | 60.6 | 222 | 2 | AAW73210 | Aaw73210 CAP37 pro |
| 15 | 66 | 60.6 | 222 | 7 | ADG42088 | Adg42088 Human pol |
| 16 | 66 | 60.6 | 225 | 2 | AAW88362 | Aaw88362 Human mat |
| 17 | 66 | 60.6 | 225 | 2 | AAY21551 | Aay21551 Human hep |
| 18 | 66 | 60.6 | 225 | 2 | AAW88118 | Aaw88118 Mature hu |
| 19 | 66 | 60.6 | 225 | 3 | AAY71881 | Aay71881 Human hep |
| 20 | 66 | 60.6 | 225 | 3 | AAY71882 | Aay71882 Human hep |
| 21 | 66 | 60.6 | 225 | 3 | AAY71883 | Aay71883 Human hep |
| 22 | 66 | 60.6 | 225 | 3 | AAY71876 | Aay71876 Human mat |
| 23 | 66 | 60.6 | 225 | 4 | AAY71891 | Aay71891 Human mat |
| 24 | 66 | 60.6 | 225 | 7 | ADE11587 | Ade11587 Human mat |
| 25 | 66 | 60.6 | 225 | 7 | ADE11551 | Ade11551 Human mat |
| 26 | 66 | 60.6 | 225 | 8 | ADK42019 | Adk42019 Human hep |
| 27 | 66 | 60.6 | 225 | 9 | ADV21099 | Adv21099 Human azu |
| 28 | 66 | 60.6 | 225 | 9 | ADX69310 | Adx69310 Human hep |
| 29 | 66 | 60.6 | 225 | 9 | ADY82139 | Ady82139 Human hep |
| 30 | 66 | 60.6 | 225 | 10 | AEJ02080 | Aej02080 Human mat |
| 31 | 66 | 60.6 | 226 | 2 | AAR10669 | Aar10669 Cationic |
| 32 | 66 | 60.6 | 228 | 7 | ADE11545 | Ade11545 Human mat |
| 33 | 66 | 60.6 | 232 | 2 | AAW88364 | Aaw88364 Human pro |
| 34 | 66 | 60.6 | 232 | 2 | AAY21550 | Aay21550 Human hep |
| 35 | 66 | 60.6 | 232 | 2 | AAW88120 | Aaw88120 Human hep |
| 36 | 66 | 60.6 | 232 | 3 | AAY71877 | Aay71877 Human pre |
| 37 | 66 | 60.6 | 232 | 10 | AEJ02083 | Aej02083 Human mat |
| 38 | 66 | 60.6 | 238 | 7 | ADE11549 | Ade11549 Human mat |
| 39 | 66 | 60.6 | 244 | 4 | AAY71893 | Aay71893 Human pre |
| 40 | 66 | 60.6 | 245 | 7 | ADE11547 | Ade11547 Human mat |
| 41 | 66 | 60.6 | 251 | 2 | AAR10668 | Aar10668 Cationic |
| 42 | 66 | 60.6 | 251 | 2 | AAR84666 | Aar84666 Human hep |
| 43 | 66 | 60.6 | 251 | 2 | AAW88365 | Aaw88365 Human pre |
| 44 | 66 | 60.6 | 251 | 2 | AAW88121 | Aaw88121 Complete |
| 45 | 66 | 60.6 | 251 | 3 | AAY71878 | Aay71878 Human pre |

ALIGNMENTS

RESULT 1

ADY21199

ID ADY21199 standard; peptide; 22 AA.

XX

AC ADY21199;

XX

DT 05-MAY-2005 (first entry)

XX

DE Human cell penetration vector peptide, DPV15b.

XX

KW cell permeabilization; virucide; antibacterial; cytostatic; vasotropic;

KW antimicrobial; antiapoptotic; antiangiogenic; pharmaceutical; cosmetics;

KW diagnostic; viral infection; metastasis; cell; vector.

XX

SCORE Search Results Details for Application 10568108 and Search Result 20070629_130905_us-10-568-108-2.rup.

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OM protein - protein search, using sw model

Run on: June 30, 2007, 00:47:37 ; Search time 343 Seconds
.. (without alignments)
.. 68.766 Million cell updates/sec

Title: US-10-568-108-2

Perfect score: 109

Sequence: 1 GAYDLRRRERQSRLRRRERQSR 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_8.4:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|--------------|---------------------|
| 1 | 66 | 60.6 | 226 | 2 | Q86SR2_HUMAN | Q86sr2 homo sapien |
| 2 | 66 | 60.6 | 251 | 1 | CAP7_HUMAN | P20160 homo sapien |
| 3 | 61 | 56.0 | 1109 | 2 | Q4BRC8_BURVI | Q4brc8 burkholderi |
| 4 | 58 | 53.2 | 785 | 2 | Q3JNU7_BURP1 | Q3jnu7 burkholderi |
| 5 | 57 | 52.3 | 386 | 2 | Q29RC7_BRARE | Q29rc7 brachydanio |
| 6 | 57 | 52.3 | 1117 | 2 | Q7RHG1_PLAYO | Q7rhg1 plasmodium |
| 7 | 55 | 50.5 | 336 | 2 | Q1LJA3_RALME | Q1lja3 ralstonia m |
| 8 | 54 | 49.5 | 77 | 1 | PRT2_SEPOF | P80002 sepiia offic |

| | | | | | | |
|----|------|------|------|---|--------------|--------------------|
| 9 | 54 | 49.5 | 167 | 2 | Q71RF1_HUMAN | Q71rf1 homo sapien |
| 10 | 54 | 49.5 | 167 | 2 | Q7Z780_HUMAN | Q7z780 homo sapien |
| 11 | 54 | 49.5 | 194 | 2 | Q9W1I6_DROME | Q9w1i6 drosophila |
| 12 | 54 | 49.5 | 227 | 2 | Q4RWW6_TETNG | Q4rww6 tetraodon n |
| 13 | 54 | 49.5 | 237 | 2 | Q98SE2_CHICK | Q98se2 gallus gall |
| 14 | 54 | 49.5 | 238 | 1 | U2AF1_MOUSE | Q9d883 mus musculu |
| 15 | 54 | 49.5 | 239 | 1 | U2AF1_HUMAN | Q01081 homo sapien |
| 16 | 54 | 49.5 | 239 | 2 | Q3KR55_RAT | Q3kr55 rattus norv |
| 17 | 54 | 49.5 | 240 | 2 | Q701P4_HUMAN | Q701p4 homo sapien |
| 18 | 54 | 49.5 | 245 | 2 | Q32NM8_XENLA | Q32nm8 xenopus lae |
| 19 | 54 | 49.5 | 973 | 2 | Q25VT3_MYCVN | Q25vt3 mycobacteri |
| 20 | 54 | 49.5 | 1450 | 2 | Q2H922_CHAGB | Q2h922 chaetomium |
| 21 | 54 | 49.5 | 1867 | 2 | Q19PP0_POPTR | Q19pp0 populus tri |
| 22 | 54 | 49.5 | 1886 | 2 | Q4SLF6_TETNG | Q4slf6 tetraodon n |
| 23 | 53.5 | 49.1 | 176 | 2 | Q5QMK8_ORYSA | Q5qmk8 oryza sativ |
| 24 | 53 | 48.6 | 60 | 1 | HSP1_MACAG | P42137 macropus ag |
| 25 | 53 | 48.6 | 61 | 1 | HSP1_MACEU | P42138 macropus eu |
| 26 | 53 | 48.6 | 175 | 1 | IF3_AQUAE | O67653 aquifex aeo |
| 27 | 53 | 48.6 | 185 | 2 | Q293G4_DROPS | Q293g4 drosophila |
| 28 | 53 | 48.6 | 227 | 2 | Q4SMD2_TETNG | Q4smd2 tetraodon n |
| 29 | 53 | 48.6 | 249 | 2 | Q8JHJ3_BRARE | Q8jhj3 brachydanio |
| 30 | 53 | 48.6 | 250 | 2 | Q4G0A1_BRARE | Q4g0a1 brachydanio |
| 31 | 53 | 48.6 | 394 | 2 | Q3JHD3_BURP1 | Q3jhd3 burkholderi |
| 32 | 53 | 48.6 | 550 | 2 | Q2QXR6_ORYSA | Q2qxr6 oryza sativ |
| 33 | 53 | 48.6 | 640 | 2 | Q2S5C1_SALRD | Q2s5c1 salinibacte |
| 34 | 53 | 48.6 | 957 | 1 | PG03_MYCTU | P56877 mycobacteri |
| 35 | 53 | 48.6 | 2002 | 2 | Q2S5B6_SALRD | Q2s5b6 salinibacte |
| 36 | 52.5 | 48.2 | 526 | 2 | Q2KG03_MAGGR | Q2kg03 magnaporthe |
| 37 | 52 | 47.7 | 63 | 1 | HSP1_HYPMS | Q9g1q1 hypsiprymno |
| 38 | 52 | 47.7 | 118 | 2 | Q7M4A3_LOLPE | Q7m4a3 loligo peal |
| 39 | 52 | 47.7 | 175 | 2 | Q5YPL2_NOCFA | Q5ypl2 nocardia fa |
| 40 | 52 | 47.7 | 285 | 2 | Q90626_CHICK | Q90626 gallus gall |
| 41 | 52 | 47.7 | 286 | 2 | Q84Q43_ORYSA | Q84q43 oryza sativ |
| 42 | 52 | 47.7 | 292 | 1 | SEN34_ASHGO | Q754t3 ashbya goss |
| 43 | 52 | 47.7 | 298 | 2 | Q292D3_DROPS | Q292d3 drosophila |
| 44 | 52 | 47.7 | 311 | 2 | Q6C9Y5_YARLI | Q6c9y5 yarrowia li |
| 45 | 52 | 47.7 | 372 | 2 | Q6DUB6_PIG | Q6dub6 sus scrofa |

ALIGNMENTS

RESULT 1

Q86SR2_HUMAN

ID Q86SR2_HUMAN PRELIMINARY; PRT; 226 AA.
 AC Q86SR2;
 DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2003, sequence version 1.
 DT 13-JUN-2006, entry version 23.
 DE AZU1 protein (Fragment).
 GN Name=AZU1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 OC Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

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OM protein - protein search, using sw model

Run on: June 30, 2007, 00:49:00 ; Search time 34 Seconds
(without alignments)
62.258 Million cell updates/sec

Title: US-10-568-108-2

Perfect score: 109

Sequence: 1. GAYDLRRRERQSLRRRERQSR 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query Score | Match | Length | DB | ID | Description |
|------------|-------------|-------|--------|----|--------|--------------------|
| 1 | 66 | 60.6 | 251 | 1 | TRHUAZ | azurocidin precurs |
| 2 | 54 | 49.5 | 77 | 2 | B40973 | spermatid-specific |
| 3 | 54 | 49.5 | 240 | 2 | A46179 | U2 snRNP auxiliary |
| 4 | 53 | 48.6 | 175 | 2 | C70453 | translation initia |
| 5 | 53 | 48.6 | 957 | 2 | D70835 | hypothetical glyci |
| 6 | 52 | 47.7 | 118 | 2 | S56117 | spermatid-specific |
| 7 | 52 | 47.7 | 285 | 2 | S53710 | ribonucleoprotein |
| 8 | 51 | 46.8 | 309 | 2 | T41889 | PE38 orf153 - Bomb |
| 9 | 51 | 46.8 | 2019 | 2 | T27702 | hypothetical prote |
| 10 | 49 | 45.0 | 43 | 2 | D58213 | protamine III - Am |
| 11 | 49 | 45.0 | 261 | 2 | AB3070 | conserved hypothet |

| | | | | | | |
|----|------|------|------|---|--------|--------------------|
| 12 | 49 | 45.0 | 319 | 2 | H98216 | hypothetical prote |
| 13 | 49 | 45.0 | 1407 | 1 | S28589 | trichohyalin - rab |
| 14 | 48 | 44.0 | 36 | 2 | JA0173 | basic peptide - wi |
| 15 | 48 | 44.0 | 234 | 2 | S27956 | arginine-rich prot |
| 16 | 48 | 44.0 | 294 | 2 | E87538 | hypothetical prote |
| 17 | 48 | 44.0 | 420 | 2 | A45166 | protein-lysine 6-o |
| 18 | 48 | 44.0 | 517 | 1 | A39038 | l-caldesmon, nonmu |
| 19 | 48 | 44.0 | 550 | 2 | A46419 | trophoblast-endoth |
| 20 | 48 | 44.0 | 695 | 2 | I54325 | gene XE7 protein - |
| 21 | 48 | 44.0 | 771 | 1 | A33430 | h-caldesmon - chic |
| 22 | 47.5 | 43.6 | 694 | 2 | T07638 | SWH1 protein homol |
| 23 | 47 | 43.1 | 27 | 1 | SRAPC | protamine B - Russ |
| 24 | 47 | 43.1 | 58 | 2 | S10755 | protamine St2b - h |
| 25 | 47 | 43.1 | 62 | 2 | S10754 | protamine St2a - h |
| 26 | 47 | 43.1 | 78 | 2 | A40973 | spermatid-specific |
| 27 | 47 | 43.1 | 79 | 2 | S56116 | spermatid-specific |
| 28 | 47 | 43.1 | 132 | 2 | S10305 | protamine - boll w |
| 29 | 47 | 43.1 | 378 | 2 | S04336 | U1 snRNP 70K prote |
| 30 | 47 | 43.1 | 406 | 2 | T24492 | hypothetical prote |
| 31 | 47 | 43.1 | 531 | 2 | A55887 | caldesmon, non-mus |
| 32 | 47 | 43.1 | 669 | 2 | JC5662 | hepatoma-derived g |
| 33 | 47 | 43.1 | 728 | 2 | T43632 | serine/threonine p |
| 34 | 47 | 43.1 | 792 | 2 | T43630 | serine/threonine p |
| 35 | 47 | 43.1 | 793 | 1 | JH0628 | caldesmon - human |
| 36 | 47 | 43.1 | 1075 | 2 | T27623 | hypothetical prote |
| 37 | 47 | 43.1 | 1080 | 2 | T27622 | hypothetical prote |
| 38 | 47 | 43.1 | 1549 | 1 | A40691 | trichohyalin - she |
| 39 | 46.5 | 42.7 | 56 | 2 | C58213 | protamine II - Ame |
| 40 | 46 | 42.2 | 126 | 2 | S58321 | probable membrane |
| 41 | 46 | 42.2 | 224 | 2 | F69444 | conserved hypothet |
| 42 | 46 | 42.2 | 321 | 1 | A43681 | immediate-early pr |
| 43 | 46 | 42.2 | 321 | 2 | C72869 | hypothetical prote |
| 44 | 46 | 42.2 | 354 | 2 | T27099 | hypothetical prote |
| 45 | 46 | 42.2 | 580 | 1 | S33743 | aspartate-tRNA lig |

ALIGNMENTS

RESULT 1

TRHUAZ

azurocidin precursor [validated] - human

N;Alternate names: cationic antimicrobial protein CAP37; heparin-binding protein; neutrophil-derive

C;Species: Homo sapiens (man)

C;Date: 31-Mar-1992 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C;Accession: A46268; A46455; S16450; S18520; S12881; S15445; S14738; B33913; A60708; B43600; A49211

R;Zimmer, M.; Medcalf, R.L.; Fink, T.M.; Mattmann, C.; Lichter, P.; Jenne, D.E.

Proc. Natl. Acad. Sci. U.S.A. 89, 8215-8219, 1992

A;Title: Three human elastase-like genes coordinately expressed in the myelomonocyte lineage are or

A;Reference number: A46268; MUID:92390417; PMID:1518849

A;Accession: A46268

A;Molecule type: DNA

A;Residues: 1-251 <ZIM>

A;Cross-references: UNIPROT:P20160; UNIPARC:UPI0000126ECD; GB:M96326; NID:g179301; PIDN:AAB59353.1;

A;Note: sequence extracted from NCBI backbone (NCBIN:112883, NCBIN:112891, NCBIN:112893, NCBIN:1128

R;Morgan, J.G.; Sukiennicki, T.; Pereira, H.A.; Spitznagel, J.K.; Guerra, M.E.; Lerrick, J.W.

J. Immunol. 147, 3210-3214, 1991

A;Title: Cloning of the cDNA for the serine protease homolog CAP37/azurocidin, a microbicidal and c

A;Reference number: A46455; MUID:92013155; PMID:1919011

A;Accession: A46455

A;Molecule type: mRNA

A;Residues: 1-251 <MOR>

A;Cross-references: UNIPARC:UPI0000126ECD; GB:M96326; NID:g179301; PIDN:AAB59353.1; PID:g179302

A;Note: sequence extracted from NCBI backbone (NCBIN:60386, NCBIP:60395)

R;Almeida, R.P.; Melchior, M.; Campanelli, D.; Nathan, C.; Gabay, J.E.

SCORE Search Results Details for Application 10568108 and Search Result 20070705_094920_us-10-568-108-1.rag.

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OM protein - protein search, using sw model

Run on: July 5, 2007, 09:49:40 ; Search time 97 Seconds
(without alignments)
80.715 Million cell updates/sec

Title: US-10-568-108-1
Perfect score: 76
Sequence: 1 LRRERQSRLRRERQSR 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : A_Geneseq_200701:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

9: geneseqp2005s:*

10: geneseqp2006s:*

11: geneseqp2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

| Result No. | Query Score | Match Length | DB ID | Description |
|------------|-------------|--------------|-------|-------------|
|------------|-------------|--------------|-------|-------------|

| | | | | | | |
|----|------|-------|------|----|----------|--------------------|
| 1 | 76 | 100.0 | 16 | 9 | ADY21198 | Ady21198 Human cel |
| 2 | 76 | 100.0 | 16 | 9 | ADY21240 | Ady21240 Gram-nega |
| 3 | 76 | 100.0 | 16 | 9 | ADY29687 | Ady29687 Antibacte |
| 4 | 76 | 100.0 | 17 | 9 | ADY21208 | Ady21208 Human cel |
| 5 | 65.5 | 86.2 | 17 | 4 | AAG67730 | Aag67730 Peptide H |
| 6 | 65.5 | 86.2 | 17 | 6 | ABP59497 | Abp59497 Human hep |
| 7 | 61.5 | 80.9 | 22 | 9 | ADY21199 | Ady21199 Human cel |
| 8 | 61.5 | 80.9 | 22 | 9 | ADY21241 | Ady21241 Gram-nega |
| 9 | 61.5 | 80.9 | 22 | 9 | ADY29688 | Ady29688 Antibacte |
| 10 | 61.5 | 80.9 | 23 | 9 | ADY21209 | Ady21209 Human cel |
| 11 | 52 | 68.4 | 476 | 4 | ABB65935 | Abb65935 Drosophil |
| 12 | 51 | 67.1 | 541 | 2 | AAW37148 | Aaw37148 Mammalian |
| 13 | 51 | 67.1 | 783 | 2 | AAW37151 | Aaw37151 Mouse neu |
| 14 | 51 | 67.1 | 787 | 2 | AAW37152 | Aaw37152 Mouse neu |
| 15 | 51 | 67.1 | 801 | 8 | ADQ97686 | Adq97686 Mouse can |
| 16 | 51 | 67.1 | 802 | 2 | AAW37153 | Aaw37153 Mouse neu |
| 17 | 51 | 67.1 | 802 | 4 | AAU09139 | Aau09139 Mammalian |
| 18 | 50 | 65.8 | 390 | 3 | AAB58287 | Aab58287 Lung canc |
| 19 | 50 | 65.8 | 467 | 7 | ADM04921 | Adm04921 Human pro |
| 20 | 50 | 65.8 | 467 | 9 | AEC87851 | Aec87851 Human cDN |
| 21 | 50 | 65.8 | 472 | 3 | AAB23039 | Aab23039 Human AVE |
| 22 | 50 | 65.8 | 472 | 6 | ADA23299 | Ada23299 Human SEC |
| 23 | 50 | 65.8 | 491 | 3 | AAB23040 | Aab23040 Human AVE |
| 24 | 50 | 65.8 | 491 | 6 | ADA23301 | Ada23301 Human SEC |
| 25 | 50 | 65.8 | 537 | 8 | ADQ97689 | Adq97689 Human can |
| 26 | 50 | 65.8 | 570 | 9 | AED84702 | Aed84702 Ponsin in |
| 27 | 50 | 65.8 | 719 | 8 | ADQ97691 | Adq97691 Human can |
| 28 | 49 | 64.5 | 1898 | 2 | AAY30795 | Aay30795 A human t |
| 29 | 49 | 64.5 | 1898 | 7 | ADD48869 | Add48869 Human Pro |
| 30 | 49 | 64.5 | 1898 | 10 | AEK65354 | Aek65354 Human tri |
| 31 | 48 | 63.2 | 70 | 9 | AEC62684 | Aec62684 PAP7 upst |
| 32 | 48 | 63.2 | 97 | 3 | AAB43257 | Aab43257 Human ORF |
| 33 | 48 | 63.2 | 126 | 8 | ADY22957 | Ady22957 Plant ful |
| 34 | 48 | 63.2 | 319 | 6 | ABU70389 | Abu70389 Human adi |
| 35 | 48 | 63.2 | 364 | 8 | ADS34465 | Ads34465 POSH prot |
| 36 | 48 | 63.2 | 364 | 8 | ADU69062 | Adu69062 Human GOC |
| 37 | 48 | 63.2 | 528 | 4 | AAM78918 | Aam78918 Human pro |
| 38 | 48 | 63.2 | 528 | 8 | ADS34467 | Ads34467 POSH prot |
| 39 | 48 | 63.2 | 528 | 8 | ADS34466 | Ads34466 POSH prot |
| 40 | 48 | 63.2 | 528 | 8 | ADS34464 | Ads34464 POSH prot |
| 41 | 48 | 63.2 | 528 | 8 | ADU69063 | Adu69063 Human GOC |
| 42 | 48 | 63.2 | 528 | 8 | ADU69061 | Adu69061 Human GOC |
| 43 | 48 | 63.2 | 528 | 8 | ADU69064 | Adu69064 Human GOC |
| 44 | 48 | 63.2 | 528 | 9 | ADX06778 | Adx06778 Cyclin-de |
| 45 | 48 | 63.2 | 545 | 4 | AAM79902 | Aam79902 Human pro |
| 46 | 47 | 61.8 | 239 | 4 | ABG16782 | Abg16782 Novel hum |
| 47 | 47 | 61.8 | 247 | 8 | ADX90684 | Adx90684 Plant ful |
| 48 | 47 | 61.8 | 247 | 8 | ADX90698 | Adx90698 Plant ful |
| 49 | 47 | 61.8 | 311 | 3 | AAB42307 | Aab42307 Human ORF |
| 50 | 47 | 61.8 | 658 | 4 | ABB65632 | Abb65632 Drosophil |

ALIGNMENTS

RESULT 1

ADY21198

ID ADY21198 standard; peptide; 16 AA.

XX

AC ADY21198;

XX

DT 05-MAY-2005 (first entry)

XX

DE Human cell penetration vector peptide, DPV15.

SCORE Search Results Details for Application 10568108 and Search Result 20070705_094922_us-10-568-108-1.rup.

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This page gives you Search Results detail for the Application 10568108 and Search Result 20070705_094922_us-10-568-108-1.rup.

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OM protein - protein search, using sw model

Run on: July 5, 2007, 09:49:44 ; Search time 353 Seconds
(without alignments)
48.595 Million cell updates/sec

Title: US-10-568-108-1
Perfect score: 76
Sequence: 1 LRRERQSRLRRERQSR 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : UniProt_8.4:*

- 1: uniprot_sprot:*
- 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|--------------|--------------------|
| 1 | 52 | 68.4 | 2753 | 2 | Q3KN34_DROME | Q3kn34 drosophila |
| 2 | 52 | 68.4 | 2935 | 2 | Q7Z1Y4_DROME | Q7z1y4 drosophila |
| 3 | 52 | 68.4 | 2946 | 2 | Q9W053_DROME | Q9w053 drosophila |
| 4 | 51 | 67.1 | 513 | 2 | Q9DEG2_CHICK | Q9deg2 gallus gall |
| 5 | 51 | 67.1 | 526 | 2 | Q5XHX3_RAT | Q5xhx3 rattus norv |
| 6 | 51 | 67.1 | 550 | 2 | O93263_CHICK | O93263 gallus gall |
| 7 | 51 | 67.1 | 784 | 2 | Q90YB5_CHICK | Q90yb5 gallus gall |
| 8 | 51 | 67.1 | 802 | 1 | ENAH_MOUSE | Q03173 mus musculu |

| | | | | | | |
|----|----|------|------|---|---------------|---------------------|
| 9 | 50 | 65.8 | 320 | 2 | Q4DK01_TRYCR | Q4dk01 trypanosoma |
| 10 | 50 | 65.8 | 391 | 2 | Q4CTG4_TRYCR | Q4ctg4 trypanosoma |
| 11 | 50 | 65.8 | 591 | 1 | ENAH_HUMAN | Q8n8s7 homo sapien |
| 12 | 49 | 64.5 | 359 | 2 | Q16LV4_AEDAE | Q16lv4 aedes aegyp |
| 13 | 49 | 64.5 | 1190 | 2 | Q519A0_ENTHI | Q519a0 entamoeba h |
| 14 | 49 | 64.5 | 1439 | 2 | Q5CQG9_CRYPV | Q5cqg9 cryptospori |
| 15 | 49 | 64.5 | 1898 | 1 | TRHY_HUMAN | Q07283 homo sapien |
| 16 | 49 | 64.5 | 1943 | 2 | Q5VUI3_HUMAN | Q5vui3 homo sapien |
| 17 | 48 | 63.2 | 260 | 2 | Q5ZD80_ORYSA | Q5zd80 oryza sativ |
| 18 | 48 | 63.2 | 372 | 2 | Q6DUB6_PIG | Q6dub6 sus scrofa |
| 19 | 48 | 63.2 | 523 | 2 | Q5RHP5_BRARE | Q5rhp5 brachydanio |
| 20 | 48 | 63.2 | 527 | 1 | GCP60_HUMAN | Q9h3p7 h golgi res |
| 21 | 48 | 63.2 | 540 | 2 | Q2J1R0_RHOP2 | Q2j1r0 rhodopseudo |
| 22 | 48 | 63.2 | 668 | 2 | Q57VZ5_9TRYR | Q57vz5 trypanosoma |
| 23 | 48 | 63.2 | 685 | 1 | CS021_PONPY | Q5rbh3 pongo pygma |
| 24 | 48 | 63.2 | 1094 | 2 | Q26774_9TRYR | Q26774 trypanosoma |
| 25 | 48 | 63.2 | 1784 | 2 | Q54TU2_DICDI | Q54tu2 dictyosteli |
| 26 | 48 | 63.2 | 1914 | 2 | Q3GJD8_CHLPH | Q3gjd8 prosthecoch |
| 27 | 47 | 61.8 | 154 | 2 | Q6YTG1_ORYSA | Q6ytg1 oryza sativ |
| 28 | 47 | 61.8 | 359 | 2 | Q5Z6A2_ORYSA | Q5z6a2 oryza sativ |
| 29 | 47 | 61.8 | 524 | 1 | GCP60_MOUSE | Q8bmp6 m golgi res |
| 30 | 47 | 61.8 | 544 | 2 | Q5B8X7_EMENI | Q5b8x7 emericella |
| 31 | 47 | 61.8 | 545 | 2 | Q4CVF8_TRYCR | Q4cvf8 trypanosoma |
| 32 | 47 | 61.8 | 545 | 2 | Q4CMJ9_TRYCR | Q4cmj9 trypanosoma |
| 33 | 47 | 61.8 | 791 | 2 | Q26LI9_XANP2 | Q26li9 xanthobacte |
| 34 | 47 | 61.8 | 800 | 2 | Q9Y102_DROME | Q9y102 drosophila |
| 35 | 47 | 61.8 | 925 | 2 | Q2QNZ9_ORYSA | Q2qnz9 oryza sativ |
| 36 | 47 | 61.8 | 971 | 2 | Q6C1S3_YARLI | Q6c1s3 yarrowia li |
| 37 | 47 | 61.8 | 1046 | 2 | Q3JNP6_BURP1 | Q3jnp6 burkholderi |
| 38 | 47 | 61.8 | 1229 | 2 | Q6C1W6_YARLI | Q6c1w6 yarrowia li |
| 39 | 47 | 61.8 | 2486 | 2 | Q9VXM5_DROME | Q9vxm5 drosophila |
| 40 | 46 | 60.5 | 117 | 2 | Q9VNS4_DROME | Q9vns4 drosophila |
| 41 | 46 | 60.5 | 129 | 2 | Q9VNS6_DROME | Q9vns6 drosophila |
| 42 | 46 | 60.5 | 289 | 1 | CWC23_SCHPO | Q9p7c6 schizosacch |
| 43 | 46 | 60.5 | 298 | 2 | Q1LZ42_DROME | Q11z42 drosophila |
| 44 | 46 | 60.5 | 399 | 2 | Q510K9_ENTHI | Q510k9 entamoeba h |
| 45 | 46 | 60.5 | 436 | 2 | Q624C9_CAEBR | Q624c9 caenorhabdi |
| 46 | 46 | 60.5 | 536 | 2 | Q50N21_ENTHI | Q50n21 entamoeba h |
| 47 | 46 | 60.5 | 537 | 2 | Q9U3Z8_ENTHI | Q9u3z8 entamoeba h |
| 48 | 46 | 60.5 | 564 | 2 | Q4SFM4_TETNG | Q4sfm4 tetraodon n |
| 49 | 46 | 60.5 | 586 | 2 | Q34WM2_9GAMM | Q34wm2 alkalilimni |
| 50 | 46 | 60.5 | 589 | 2 | Q1EA13_CO CIM | Q1ea13 coccidioides |

ALIGNMENTS

RESULT 1

Q3KN34_DROME
 ID Q3KN34_DROME PRELIMINARY; PRT; 2753 AA.
 AC Q3KN34;
 DT 08-NOV-2005, integrated into UniProtKB/TrEMBL.
 DT 08-NOV-2005, sequence version 1.
 DT 18-APR-2006, entry version 5.
 DE GH18167p (Fragment).
 GN Name=CG33484-RA;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydriidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1].
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Berkeley;
 RA Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,

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This page gives you Search Results detail for the Application 10568108 and Search Result 20070705_094924_us-

GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: July 5, 2007, 09:50:55 ; Search time 31 Seconds
(without alignments)
49.660 Million cell updates/sec

Title: US-10-568-108-1

Perfect score: 76

Sequence: 1 LRRERQSRLRRERQSR 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : PIR_80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB | ID | Description |
|------------|-------|-------|--------|----|--------|--------------------|
| 1 | 49 | 64.5 | 1898 | 1 | A45973 | trichohyalin - hum |
| 2 | 48 | 63.2 | 1094 | 2 | A53435 | vesicular transpor |
| 3 | 46 | 60.5 | 675 | 2 | D83405 | conserved hypothet |
| 4 | 46 | 60.5 | 699 | 2 | E84565 | hypothetical prote |
| 5 | 45 | 59.2 | 1027 | 2 | T46481 | hypothetical prote |
| 6 | 45 | 59.2 | 1233 | 2 | T30989 | serine/threonine p |
| 7 | 45 | 59.2 | 3498 | 2 | T22330 | hypothetical prote |
| 8 | 44 | 57.9 | 36 | 2 | JA0173 | basic peptide - wi |
| 9 | 44 | 57.9 | 263 | 2 | B84778 | hypothetical prote |
| 10 | 44 | 57.9 | 454 | 2 | T19433 | hypothetical prote |
| 11 | 44 | 57.9 | 679 | 2 | T00636 | hypothetical prote |

| | | | | | | |
|----|----|------|------|---|--------|--------------------|
| 12 | 44 | 57.9 | 1407 | 1 | S28589 | trichohyalin - rab |
| 13 | 43 | 56.6 | 118 | 2 | S56117 | spermatid-specific |
| 14 | 43 | 56.6 | 308 | 2 | F95416 | hypothetical prote |
| 15 | 43 | 56.6 | 413 | 2 | H88481 | protein let-756 [i |
| 16 | 43 | 56.6 | 427 | 2 | AE2512 | hypothetical prote |
| 17 | 43 | 56.6 | 444 | 2 | T32648 | hypothetical prote |
| 18 | 43 | 56.6 | 468 | 1 | FOMVMU | gag polyprotein - |
| 19 | 43 | 56.6 | 538 | 1 | FOMVM | gag polyprotein - |
| 20 | 43 | 56.6 | 569 | 2 | T43531 | probable potassium |
| 21 | 43 | 56.6 | 733 | 2 | G84668 | hypothetical prote |
| 22 | 43 | 56.6 | 1175 | 2 | T22491 | hypothetical prote |
| 23 | 42 | 55.3 | 58 | 2 | S34045 | protamine - North |
| 24 | 42 | 55.3 | 78 | 2 | A40973 | spermatid-specific |
| 25 | 42 | 55.3 | 79 | 2 | S56116 | spermatid-specific |
| 26 | 42 | 55.3 | 99 | 2 | B46598 | ski-related protei |
| 27 | 42 | 55.3 | 126 | 2 | S58321 | probable membrane |
| 28 | 42 | 55.3 | 296 | 2 | S73007 | hypothetical prote |
| 29 | 42 | 55.3 | 513 | 2 | T03916 | hypothetical prote |
| 30 | 42 | 55.3 | 614 | 2 | AB2304 | two-component hybr |
| 31 | 42 | 55.3 | 684 | 1 | TVHUSN | transforming prote |
| 32 | 42 | 55.3 | 690 | 2 | I51298 | transforming prote |
| 33 | 42 | 55.3 | 704 | 2 | T24517 | hypothetical prote |
| 34 | 42 | 55.3 | 710 | 2 | AE1956 | hypothetical prote |
| 35 | 42 | 55.3 | 737 | 2 | T15597 | hypothetical prote |
| 36 | 42 | 55.3 | 749 | 2 | T08101 | outer dynein arm d |
| 37 | 42 | 55.3 | 788 | 2 | G89901 | hypothetical prote |
| 38 | 42 | 55.3 | 810 | 2 | T44430 | protein PV100 [imp |
| 39 | 42 | 55.3 | 919 | 2 | F81998 | ribonuclease E (EC |
| 40 | 42 | 55.3 | 919 | 2 | F81225 | ribonuclease E NMB |
| 41 | 42 | 55.3 | 1017 | 2 | T15598 | hypothetical prote |
| 42 | 42 | 55.3 | 1131 | 2 | S22266 | FUN30 protein - ye |
| 43 | 42 | 55.3 | 2550 | 2 | B53435 | vesicular transpor |
| 44 | 41 | 53.9 | 45 | 2 | B58208 | protamine II-1 - p |
| 45 | 41 | 53.9 | 47 | 2 | F58208 | protamine II-5 - p |
| 46 | 41 | 53.9 | 47 | 2 | E58208 | protamine II-4 - p |
| 47 | 41 | 53.9 | 142 | 2 | B72667 | hypothetical prote |
| 48 | 41 | 53.9 | 227 | 2 | T46264 | hypothetical prote |
| 49 | 41 | 53.9 | 279 | 2 | T26166 | hypothetical prote |
| 50 | 41 | 53.9 | 325 | 2 | H96815 | hypothetical prote |

ALIGNMENTS

RESULT 1

A45973

trichohyalin - human

C;Species: Homo sapiens (man)

C;Date: 03-May-1994 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004

C;Accession: A45973

R;Lee, S.C.; Kim, I.G.; Marekov, L.N.; O'Keefe, E.J.; Parry, D.A.D.; Steinert, P.M.

J. Biol. Chem. 268, 12164-12176, 1993

A;Title: The structure of human trichohyalin. Potential multiple roles as a functional EF-hand-like

A;Reference number: A45973; MUID:93280194; PMID:7685034

A;Accession: A45973

A;Molecule type: DNA

A;Residues: 1-1898 <LEE>

A;Cross-references: UNIPROT:Q07283; UNIPARC:UPI000013738B; GB:L09190; NID:g292835; PIDN:AAA65582.1;

A;Note: authors translated the codon AGG for residue 1714 as Pro

C;Comment: Trichohyalin is a protein of the medulla of the hair and of the inner root sheath cells

C;Genetics:

A;Gene: GDB:THH

A;Cross-references: GDB:136223; OMIM:190370

A;Map position: 1q21-1q21

C;Superfamily: trichohyalin; calmodulin repeat homology

conjugation of a short polylysine tail converted a spontaneously internalizing peptide into a potent nontoxic plasmid vector.

REFERENCE COUNT: 39 THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 4 OF 11 ZCAPIUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 1998:311775 ZCAPIUS Full-text
DOCUMENT NUMBER: 122:80189
TITLE: Polyreactive anti-DNA monoclonal antibodies and a derived peptide as vectors for the intracytoplasmic and intranuclear translocation of macromolecules

AUTHOR(S): Avrameas, Alexandre; Tirmenck, Therese; Nato, Faridabano; Buttin, Gerard; Avrameas, Stratis
CORPORATE SOURCE: Unité de Génétique Somatique, Département de Biotechnologie, Institut Pasteur, Paris, 75015, Fr. Proceedings of the National Academy of Sciences of the United States of America (1998), 95(10), 5601-5605
CODEN: PNASAA; ISSN: 0027-8424
PUBLISHER: National Academy of Sciences
DOCUMENT TYPE: Journal

LANGUAGE: English
AB Naturally occurring polyreactive anti-DNA mabs derived from a nonimmunized (NZB + NZW)F1 mouse with spontaneous lupus erythematosus penetrated and accumulated in the nuclei of a variety of cultured cells. These mabs and their F(ab')2 and Fab' fragments, covalently coupled to fluorescein, peroxidase, or a 15-mer polynucleotide, also translocated to the cell nuclei.

A 30-amino acid peptide corresponding to the combined sequences of the complementary-determining regions 2 and 3 of the heavy chain variable region of one mAb was able to penetrate into the cytoplasm and nucleus of cells of several lines. This peptide recognized DNA and was strongly polyreactive. Streptavidin-peroxidase conjugates complexed with the N-biotinylated peptide were rapidly translocated into cells. Similarly, peroxidase or anti-peroxidase polyclonal antibodies covalently coupled to the N-cysteinylditid peptide through an heterobifunctional maleimide cross-linker were also rapidly internalized and frequently accumulated in nuclei. The peptide carrying 19 lysine residues at its N-terminal was highly effective in transfecting 3T3 cells with a plasmid containing the luciferase gene. Thus, penetrating mabs and derived peptides are versatile vectors for the intracellular delivery of proteins and genes.

REFERENCE COUNT: 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 5 OF 11 ZCAPIUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 1997:312328 ZCAPIUS Full-text
DOCUMENT NUMBER: 127:134458
TITLE: Mimotopes of polyreactive anti-DNA antibodies identified using phage-display peptide libraries
AUTHOR(S): Sibille, Pierre; Ternynck, Therese; Nato, Faridabano; Buttin, Gerard; Strosberg, Donny; Avrameas, Alexandre
CORPORATE SOURCE: Institut Cochin Génétique Moléculaire, Paris, Fr. European Journal of Immunology (1997), 27(5), 1221-1228
CODEN: EJIMAF; ISSN: 0014-2980
VCH
PUBLISHER: Journal

LANGUAGE: English
AB Three monoclonal IgG2a anti-DNA polyreactive autoantibodies, derived from lupus-prone mice (NZB + NZW)F1, were studied by surface plasmon resonance (BIAcore) anal. using 3 different synthetic double-stranded (ds)

oligonucleotides of 25, 30, and 25 base pairs (bp). These monoclonal antibodies (mAb) exhibited dissociation rate constants, (k_{off}) ranging from 0.0011 (mAb F14.6 and F4.11) to 0.01/s (mAb J20.8) and kon ranging from 2.105 to 2.106 /M/s. The screening of a constrained random peptide library displayed on M13-bacteriophages on these mAb allowed the determination of the specific consensus motifs (mimotopes) for mab F14.6 and J20.8, but not for mab F4.1. No cross-reaction was observed between F14.6- and J20.8-specific peptides (and vice versa). Binding of all phages selected on F14.6 was inhibited with 700 ng/mL soluble DNA. The binding of a group of peptides selected on J20.8 was inhibited by 400 ng/mL soluble DNA, of a 2nd group by 2500 ng/mL, while binding of a 3rd group was not inhibited. The determined consensus sequences do not match with known sequences. Peptides specific for F14.6 share neg. charges and aromatic rings that may mimic a DNA backbone, while peptides selected on J20.8 do not bear any neg. charge, implying a different kind of mol. recognition, for example hydrogen or salt bonds. The peptides selected on J20.8 also bind serum antibodies from human patients with systemic lupus erythematosus. BALB/c mice immunized with some of the selected phages exhibit high serum titers of IgG3 anti-dsDNA antibodies, further supporting the hypothesis that peptide epitopes may mimic an oligonucleotide structure.

L13 ANSWER 6 OF 11 ZCAPIUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 1996:181560 ZCAPIUS Full-text
DOCUMENT NUMBER: 124:230006

Peptide fragment specific for feline immunodeficiency virus (FIV) and its use as a diagnostic reagent for antibody detection and disease diagnosis

INVENTOR(S): Avrameas, Alexandre; Pancino, Gianfranco; Sibille, Pierre; Sonigo, Pierre; Strosberg, Arthur Donny Centre National de la Recherche Scientifique (CNRS), Fr. Bur. Pat. Appl., 12 pp.
DOCUMENT TYPE: Patent
LANGUAGE: French
PATENT ASSIGNEE(S):
PATENT INFO: FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|------|----------|-----------------|------------|
| EP 688790 | A1 | 19951227 | EP 1995-401316 | 19950607 |
| R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE | A1 | 19951215 | FR 1994-7062 | 19940609 |
| FR 2721031 | B1 | 19960726 | | |
| FR 2721031 | A | 19970715 | US 1995-487485 | 19950607 |
| US 5643209 | | | FR 1994-7062 | A 19940609 |

PRIORITY APPLN. INFO.: A peptide fragment P253 was prepared from the Env protein of feline immunodeficiency virus W6 strain, derived from positions 693-709 of the protein, wherein the 3rd and/or 10th residues are replaced with cysteine or serine. The peptide is used to detect antibodies to the virus in biological fluids as a diagnostic kit. The peptide proved more sensitive in a comparative ELISA than did P237.

L13 ANSWER 7 OF 11 ZCAPIUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 1996:111032 ZCAPIUS Full-text
DOCUMENT NUMBER: 124:143569
TITLE: Expression of a mannose/fucose membrane lectin on

AUTHOR(S): Armanas, Alexandre; McIlroy, Dorian;
Hosmalin, Anne; Autran, Brigitte; Debrie, Patrice;
Monsigny, Michel; Roche, Annie Claude; Midoux, Patricia;
CORPORATE SOURCE: Glycobil, Cent Biophysique Moléculaire, CNRS, Univ.
d'Orléans, Orleans, FR.

PUBLISHER: CODEN: EIJMAF, ISSN: 0014-2980
DOCUMENT TYPE: VCH
Journal

Dendritic cells (DC) are the most efficient antigen presenting cells for T lymphocytes. CD14+ DC with high antigen-presenting capacities can now be obtained easily from adherent peripheral blood monocytes by culture in the presence of granulocyte/macrophage colony-stimulating factor and interleukin-4 (Sallusto et al., 1994). Human macrophages express a membrane lectin, or sugar-specific receptor, which specifically mediates the binding and

| AB | | Nucleotide and protein sequences from feline immunodeficiency virus 'wo' are identified and the genes used to manufacture viral peptides for use in diagnostics and prophylaxis, e.g. vaccines. Specifically, the env and gag genes and gene products are characterized as are the SU and TM epitopes of the env protein. Sequences were cloned from peripheral blood lymphocytes of infected animals by PCR using primers derived from the corresponding sequences of the Petaluma isolate. These sequences were used to construct full-length copies of the genes. Sequence divergence between the Petaluma and WO isolates were sufficient to differentiate the strains by hybridization. Immunodominant epitopes of the env protein were used in the diagnosis of infection. | | |
|-----------------|---------|--|---------------|------------|
| FR 2622269 | BL | 19950519 | | |
| FR 2622270 | A1 | 19931217 | FR 1992-14026 | 19921123 |
| AT 270018 | T | 20041015 | AT 1993-01138 | 19930016 |
| PRIORITY APPLN. | INFO. : | | FR 1992-257 | A 19920616 |
| | | | FR 1992-7258 | A 19920616 |
| | | | FR 1992-14026 | A 19921123 |

the phagocytosis of pathogens. A similar lectin activity was sought on cultured human DC using flow cytometry and confocal microscopy to detect binding and internalization of fluoresceinated neoglycoproteins [bovine serum albumin (BSA) substituted with sugar residues]. Several neoglycoproteins, especially α -L-fucosyl-, α -D-mannosyl-, N,N-di-acetyl- β -D-glucosyl- and β -D-glucosyl-BSA, were endocytosed by cultured human CD1a+ DC as well as by CD1a- cells which were also obtained in the culture. Fuc-BSA and Man-BSA had the same number of binding sites ($1.7 \pm 105/\text{cell}$) on CD1a+ DC, and bound with an affinity constant close to 107 M^{-1} . Inhibition experiments indicated that both these two neoglycoproteins bound to the same membrane lectin. CD1a+ and CD1a- cells were both labeled with an antiserum specific for the human macrophage mannose receptor. The membrane lectin specific for mannose and fucose that is

membrane lectin or may share functional and structural properties with it.

ACCESSION NUMBER: 1994-240106 ZC48955 Full-text
DOCUMENT NUMBER: 120-240106
TITLE: Gene and protein sequence from the WO isolate of feline immunodeficiency virus and their use in diagnosis and prophylaxis of infection
INVENTOR(S): Pancino, Gianfranco; Chappay, Colombe; Hurtrel, Bruno; Morailon, Anne; Klatzmann, David; Sonigo, Pierre;
Saurin, William; Armaeas, Alexandre;
Stroesberg, Arthur Donny
Centre National de la Recherche Scientifique, Fr.
PATENT ASSIGNEE(S): Eur. Pat. Appl., 56 pp.
SOURCE: CODEN: EPPXDN

LANGUAGE: French
FAMILY ACC. NUM. COUNT: 1

| PATENT INFORMATION: | | PATENT NO. | | KIND | DATE | APPLICATION NO. | DATE |
|---------------------|----------|---|---|------|----------|-----------------|----------|
| LANGUAGE: | English | EP 577458 | EP 577458 | A1 | 19900105 | EP 1991-401538 | 19930616 |
| FAMILY ACC. | 1 Family | R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE | R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE | B1 | 20040929 | | |
| NUM. COUNT: | 1 | FR 2622279 | FR 2622279 | A1 | 19931217 | FR 1992-7257 | 19920616 |
| | | FR 2622279 | FR 2622279 | B1 | 19950519 | | |
| | | FR 2622269 | FR 2622269 | A1 | 19931217 | FR 1992-7258 | 19920616 |